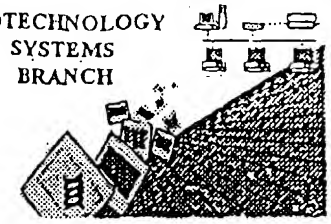
BIOTECHNOLOGY SYSTEMS BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/031,496B
Source: IFW16 -
Date Processed by STIC: 3/12/04 -

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221
Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for UR disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>, EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 4B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED | SUGGESTED CORRECTION | SERIAL NUMBER: 10/031,4963

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1	Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2	Invalid Line Length	The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
3	Misaligned Amino Numbering	The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use **space characters**, instead.
4	Non-ASCII	The **submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.**
5	Variable Length	Sequence(s)____contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6	PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
7	Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for **each** skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
8	Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. **If intentional**, please insert the following lines for **each** skipped sequence. <210> sequence id number <400> sequence id number 000
9	Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
10	Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11	Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
12	PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
13	Misuse of n/Xaa	"n" can **only** represent a single nucleotide; "Xaa" can only represent a single amino acid

IFW16

RAW SEQUENCE LISTING DATE: 03/12/2004
PATENT APPLICATION: **US/10/031,496B** TIME: 14:56:14

Input Set : **A:\NREL 99-45.ST25.txt**
Output Set: **N:\CRF4\03122004\J031496B.raw**

```
 3 <110> APPLICANT: National Renewable Energy Laboratory
 5 <120> TITLE OF INVENTION: Cellobiohydrolase I Gene and Improved Variants
 7 <130> FILE REFERENCE: NREL 99-45
 9 <140> CURRENT APPLICATION NUMBER: 10/031,496B
10 <141> CURRENT FILING DATE: 2002-01-14
12 <160> NUMBER OF SEQ ID NOS: 120
14 <170> SOFTWARE: PatentIn version 3.2
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 28
18 <212> TYPE: DNA
19 <213> ORGANISM: Synthetic DNA
21 <400> SEQUENCE: 1
22 agagagtcta gacacggagc ttacaggc                                        28
25 <210> SEQ ID NO: 2
26 <211> LENGTH: 35
27 <212> TYPE: DNA
28 <213> ORGANISM: Synthetic DNA
30 <400> SEQUENCE: 2
31 aaagaagcgc ggccgcgcct gcactctcca atcgg                                35
34 <210> SEQ ID NO: 3
35 <211> LENGTH: 24
36 <212> TYPE: DNA
37 <213> ORGANISM: Synthetic DNA
39 <400> SEQUENCE: 3
40 ggcggaaacc cgcctggcac cacc                                            24
43 <210> SEQ ID NO: 4
44 <211> LENGTH: 1550
45 <212> TYPE: DNA
46 <213> ORGANISM: Trichoderma reesei
49 <220> FEATURE:
50 <221> NAME/KEY: misc_signal
51 <222> LOCATION: (1)..(51)
53 <220> FEATURE:
54 <221> NAME/KEY: CDS
55 <222> LOCATION: (3)..(1550)
57 <220> FEATURE:
58 <221> NAME/KEY: misc_feature
59 <222> LOCATION: (52)..(1344)
61 <220> FEATURE:
62 <221> NAME/KEY: misc_feature
63 <222> LOCATION: (1345)..(1435)
65 <220> FEATURE:
66 <221> NAME/KEY: misc_binding
```

invalid <213> response see item 10 on Error Summary Sheet

Sep. 6, 2004

Please correct this error in subsequent sequences, if present.

RAW SEQUENCE LISTING DATE: 03/12/2004
PATENT APPLICATION: US/10/031,496B TIME: 14:56:14

Input Set : A:\NREL 99-45.ST25.txt
Output Set: N:\CRF4\03122004\J031496B.raw

```
67 <222> LOCATION: (1436)..(1550)
69 <400> SEQUENCE: 4
70 at gta tcg gaa gtt ggc cgt cat ctc ggc ctt ctt ggc cac agc tcg        47
71    Val Ser Glu Val Gly Arg His Leu Gly Leu Leu Gly His Ser Ser
72    1               5                  10                  15
74 tgc tca gtc ggc ctg cac tct cca atc gga gac tca ccc gcc tct gac        95
75 Cys Ser Val Gly Leu His Ser Pro Ile Gly Asp Ser Pro Ala Ser Asp
76                 20                  25                  30
78 atg gca gaa atg ctc gtc tgg tgg cac gtg cac tca aca gac agg ctc       143
79 Met Ala Glu Met Leu Val Trp Trp His Val His Ser Thr Asp Arg Leu
80             35                  40                  45
82 cgt ggt cat cga cgc caa ctg gcg ctg gac tca cgc tac gaa cag cag       191
83 Arg Gly His Arg Arg Gln Leu Ala Leu Asp Ser Arg Tyr Glu Gln Gln
84         50                  55                  60
86 cac gaa ctg cta cga tgg caa cac ttg gag ctc gac cct atg tcc tga       239
87 His Glu Leu Leu Arg Trp Gln His Leu Glu Leu Asp Pro Met Ser
88     65                  70                  75
90 caa cga gac ctg cgc gaa gaa ctg ctg tct gga cgg tgc cgc cta cgc       287
91 Gln Arg Asp Leu Arg Glu Glu Leu Leu Ser Gly Arg Cys Arg Leu Arg
92     80                  85                  90
94 gtc cac gta cgg agt tac cac gag cgg taa cag cct ctc cat tgg ctt       335
95 Val His Val Arg Ser Tyr His Glu Arg     Gln Pro Leu His Trp Leu
96 95                  100                 105
98 tgt cac cca gtc tgc gca gaa gaa cgt tgg cgc tcg cct tta cct tat       383
99 Cys His Pro Val Cys Ala Glu Glu Arg Trp Arg Ser Pro Leu Pro Tyr
100 110                 115                 120                 125
102 ggc gag cga cac gac cta cca gga att cac cct gct tgg caa cga gtt      431
103 Gly Glu Arg His Asp Leu Pro Gly Ile His Pro Ala Trp Gln Arg Val
104                 130                 135                 140
106 ctc ttt cga tgt tga tgt ttc gca gct gcc gtg cgg ctt gaa cgg agc      479
107 Leu Phe Arg Cys     Cys Phe Ala Ala Ala Val Arg Leu Glu Arg Ser
108             145                 150                 155
110 tct cta ctt cgt gtc cat gga cgc gga tgg tgg cgt gag caa gta tcc      527
111 Ser Leu Leu Arg Val His Gly Arg Gly Trp Trp Arg Glu Gln Val Ser
112             160                 165                 170
114 cac caa cac cgc tgg cgc caa gta cgg cac ggg gta ctg tga cag cca      575
115 His Gln His Arg Trp Arg Gln Val Arg His Gly Val Leu     Gln Pro
116         175                 180                 185
118 gtg tcc ccg cga tct gaa gtt cat caa tgg cca ggc caa cgt tga ggg      623
119 Val Ser Pro Arg Ser Glu Val His Gln Trp Pro Gly Gln Arg     Gly
120         190                 195                 200
122 ctg gga gcc gtc atc caa caa cgc gaa cac ggg cat tgg agg aca cgg      671
123 Leu Gly Ala Val Ile Gln Gln Arg Glu His Gly His Trp Arg Thr Arg
124         205                 210                 215
126 aag ctg ctg ctc tga gat gga tat ctg gga ggc caa ctc cat ctc cga      719
127 Lys Leu Leu Leu     Asp Gly Tyr Leu Gly Gly Gln Leu His Leu Arg
128     220                 225                 230
130 ggc tct tac ccc cca ccc ttg cac gac tgt cgg cca gga gat ctg cga      767
131 Gly Ser Tyr Pro Pro Pro Leu His Asp Cys Arg Pro Gly Asp Leu Arg
```

RAW SEQUENCE LISTING DATE: 03/12/2004
PATENT APPLICATION: US/10/031,496B TIME: 14:56:14

Input Set : A:\NREL 99-45.ST25.txt
Output Set: N:\CRF4\03122004\J031496B.raw

```
132      235                 240                 245
134 ggg tga tgg gtg cgg cgg aac tta ctc cga taa cag ata tgg cgg cac      815
135 Gly     Trp Val Arg Arg Asn Leu Leu Arg     Gln Ile Trp Arg His
136 250                 255                 260
138 ttg cga tcc cga tgg ctg cga ctg gaa ccc ata ccg cct ggg caa cac      863
139 Leu Arg Ser Arg Trp Leu Arg Leu Glu Pro Ile Pro Pro Gly Gln His
140      265                 270                 275
142 cag ctt cta cgg ccc tgg ctc aag ctt tac cct cga tac cac caa gaa      911
143 Gln Leu Leu Arg Pro Trp Leu Lys Leu Tyr Pro Arg Tyr His Gln Glu
144 280                 285                 290                 295
146 att gac cgt tgt cac cca gtt cga gac gtc ggg tgc cat caa ccg ata      959
147 Ile Asp Arg Cys His Pro Val Arg Asp Val Gly Cys His Gln Pro Ile
148                 300                 305                 310
150 cta tgt cca gaa tgg cgt cac ttt cca gca gcc caa cgc cga gct tgg     1007
151 Leu Cys Pro Glu Trp Arg His Phe Pro Ala Ala Gln Arg Arg Ala Trp
152                 315                 320                 325
154 tag tta ctc tgg caa cga gct caa cga tga tta ctg cac agc tga gga     1055
155     Leu Leu Trp Gln Arg Ala Gln Arg     Leu Leu His Ser     Gly
156                 330                 335                 340
158 ggc aga att cgg cgg atc ctc ttt ctc aga caa ggg cgg cct gac tca     1103
159 Gly Arg Ile Arg Arg Ile Leu Phe Leu Arg Gln Gly Arg Pro Asp Ser
160                 345                 350                 355
162 gtt caa gaa ggc tac ctc tgg cgg cat ggt tct ggt cat gag tct gtg     1151
163 Val Gln Glu Gly Tyr Leu Trp Arg His Gly Ser Gly His Glu Ser Val
164                 360                 365                 370
166 gga tga tta cta cgc caa cat gct gtg gct gga ctc cac cta ccc gac     1199
167 Gly     Leu Leu Arg Gln His Ala Val Ala Gly Leu His Leu Pro Asp
168                 375                 380                 385
170 aaa cga gac ctc ctc cac acc cgg tgc cgt gcg cgg aag ctg ctc cac     1247
171 Lys Arg Asp Leu Leu His Thr Arg Cys Arg Ala Arg Lys Leu Leu His
172         390                 395                 400
174 cag ctc cgg tgt ccc tgc tca ggt cga atc tca gtc tcc caa cgc caa     1295
175 Gln Leu Arg Cys Pro Cys Ser Gly Arg Ile Ser Val Ser Gln Arg Gln
176     405                 410                 415
178 ggt cac ctt ctc caa cat caa gtt cgg acc cat tgg cag cac cgg caa     1343
179 Gly His Leu Leu Gln His Gln Val Arg Thr His Trp Gln His Arg Gln
180 420                 425                 430                 435
182 ccc tag cgg cgg caa ccc tcc cgg cgg aaa ccc gcc tgg cac cac cac     1391
183 Pro     Arg Arg Gln Pro Ser Arg Arg Lys Pro Ala Trp His His His
184                 440                 445                 450
186 cac ccg ccg ccc agc cac tac cac tgg aag ctc tcc cgg acc tac cca     1439
187 His Pro Pro Pro Ser His Tyr His Trp Lys Leu Ser Arg Thr Tyr Pro
188                 455                 460                 465
190 gtc tca cta cgg cca gtg cgg cgg tat tgg cta cag cgg ccc cac ggt     1487
191 Val Ser Leu Arg Pro Val Arg Arg Tyr Trp Leu Gln Arg Pro His Gly
192             470                 475                 480
194 ctg cgc cag cgg cac aac ttg cca ggt cct gmc cct tac tac tct cag     1535
195 Leu Arg Gln Arg His Asn Leu Pro Gly Pro Xaa Pro Tyr Tyr Ser Gln
196         485                 490                 495
```

RAW SEQUENCE LISTING DATE: 03/12/2004
PATENT APPLICATION: US/10/031,496B TIME: 14:56:14

Input Set : A:\NREL 99-45.ST25.txt
Output Set: N:\CRF4\03122004\J031496B.raw

```
198 tgc ctg taa agc tcc                                                 1550
199 Cys Leu     Ser Ser
200     500
203 <210> SEQ ID NO: 5
204 <211> LENGTH: 78
205 <212> TYPE: PRT
206 <213> ORGANISM: Trichoderma reesei
208 <400> SEQUENCE: 5
210 Val Ser Glu Val Gly Arg His Leu Gly Leu Leu Gly His Ser Ser Cys
211 1               5                   10                  15
214 Ser Val Gly Leu His Ser Pro Ile Gly Asp Ser Pro Ala Ser Asp Met
215             20                  25                  30
218 Ala Glu Met Leu Val Trp Trp His Val His Ser Thr Asp Arg Leu Arg
219         35                  40                  45
222 Gly His Arg Arg Gln Leu Ala Leu Asp Ser Arg Tyr Glu Gln Gln His
223     50                  55                  60
226 Glu Leu Leu Arg Trp Gln His Leu Glu Leu Asp Pro Met Ser
227 65                  70                  75
230 <210> SEQ ID NO: 6
231 <211> LENGTH: 25
232 <212> TYPE: PRT
233 <213> ORGANISM: Trichoderma reesei
235 <400> SEQUENCE: 6
237 Gln Arg Asp Leu Arg Glu Glu Leu Leu Ser Gly Arg Cys Arg Leu Arg
238 1               5                   10                  15
241 Val His Val Arg Ser Tyr His Glu Arg
242             20                  25
245 <210> SEQ ID NO: 7
246 <211> LENGTH: 42
247 <212> TYPE: PRT
248 <213> ORGANISM: Trichoderma reesei
250 <400> SEQUENCE: 7
252 Gln Pro Leu His Trp Leu Cys His Pro Val Cys Ala Glu Glu Arg Trp
253 1               5                   10                  15
256 Arg Ser Pro Leu Pro Tyr Gly Glu Arg His Asp Leu Pro Gly Ile His
257             20                  25                  30
260 Pro Ala Trp Gln Arg Val Leu Phe Arg Cys
261         35                  40
264 <210> SEQ ID NO: 8
265 <211> LENGTH: 40
266 <212> TYPE: PRT
267 <213> ORGANISM: Trichoderma reesei
269 <400> SEQUENCE: 8
271 Cys Phe Ala Ala Ala Val Arg Leu Glu Arg Ser Ser Leu Leu Arg Val
272 1               5                   10                  15
275 His Gly Arg Gly Trp Trp Arg Glu Gln Val Ser His Gln His Arg Trp
276             20                  25                  30
279 Arg Gln Val Arg His Gly Val Leu
280         35                  40
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RAW SEQUENCE LISTING DATE: 03/12/2004
PATENT APPLICATION: US/10/031,496B TIME: 14:56:14

Input Set : A:\NREL 99-45.ST25.txt
Output Set: N:\CRF4\03122004\J031496B.raw

```
283 <210> SEQ ID NO: 9
284 <211> LENGTH: 16
285 <212> TYPE: PRT
286 <213> ORGANISM: Trichoderma reesei
288 <400> SEQUENCE: 9
290 Gln Pro Val Ser Pro Arg Ser Glu Val His Gln Trp Pro Gly Gln Arg
291 1               5                   10                  15
294 <210> SEQ ID NO: 10
295 <211> LENGTH: 21
296 <212> TYPE: PRT
297 <213> ORGANISM: Trichoderma reesei
299 <400> SEQUENCE: 10
301 Gly Leu Gly Ala Val Ile Gln Gln Arg Glu His Gly His Trp Arg Thr
302 1               5                   10                  15
305 Arg Lys Leu Leu Leu
306             20
309 <210> SEQ ID NO: 11
310 <211> LENGTH: 28
311 <212> TYPE: PRT
312 <213> ORGANISM: Trichoderma reesei
314 <400> SEQUENCE: 11
316 Asp Gly Tyr Leu Gly Gly Gln Leu His Leu Arg Gly Ser Tyr Pro Pro
317 1               5                   10                  15
320 Pro Leu His Asp Cys Arg Pro Gly Asp Leu Arg Gly
321             20                  25
324 <210> SEQ ID NO: 12
325 <211> LENGTH: 8
326 <212> TYPE: PRT
327 <213> ORGANISM: Trichoderma reesei
329 <400> SEQUENCE: 12
331 Trp Val Arg Arg Asn Leu Leu Arg
332 1               5
335 <210> SEQ ID NO: 13
336 <211> LENGTH: 69
337 <212> TYPE: PRT
338 <213> ORGANISM: Trichoderma reesei
340 <400> SEQUENCE: 13
342 Gln Ile Trp Arg His Leu Arg Ser Arg Trp Leu Arg Leu Glu Pro Ile
343 1               5                   10                  15
346 Pro Pro Gly Gln His Gln Leu Leu Arg Pro Trp Leu Lys Leu Tyr Pro
347             20                  25                  30
350 Arg Tyr His Gln Glu Ile Asp Arg Cys His Pro Val Arg Asp Val Gly
351         35                  40                  45
354 Cys His Gln Pro Ile Leu Cys Pro Glu Trp Arg His Phe Pro Ala Ala
355     50                  55                  60
358 Gln Arg Arg Ala Trp
359 65
362 <210> SEQ ID NO: 14
363 <211> LENGTH: 8
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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 03/12/2004
PATENT APPLICATION: US/10/031,496B TIME: 14:56:15

Input Set : A:\NREL 99-45.ST25.txt
Output Set: N:\CRF4\03122004\J031496B.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; Xaa Pos. 493
Seq#:18; Xaa Pos. 57
Seq#:32; Xaa Pos. 57

VERIFICATION SUMMARY DATE: 03/12/2004
PATENT APPLICATION: **US/10/031,496B** TIME: 14:56:15

Input Set : **A:\NREL 99-45.ST25.txt**
Output Set: **N:\CRF4\03122004\J031496B.raw**

L:195 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ ID#:4
L:195 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:1535
L:450 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:48
L:702 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:32 after pos.:48